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OM nucleic - nucleic search, using sw model

Run on: June 8, 2003, 18:16:33 ; Search time 300 Seconds
(without alignments)
8512.554 Million cell updates/sec

Title: US-10-091-628-1

Perfect score: 1134
Sequence: 1 atgagagcaccatgttcacg.....acatcactcatgcatag 1134

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Indexed: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : N Geneseq_101002.*

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3: /SID82/gcgdata/geneseq/geneeqn-emb1/NA1982.DAT.*
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23: /SID82/gcgdata/geneseq/geneeqn-emb1/NA2001B.DAT.*
24: /SID82/gcgdata/geneseq/geneeqn-emb1/NA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	320.4	28.3	2263	16	AAO91108	Hamster ileal/rena
2	297.8	26.3	1047	16	AAO91109	Human ileal/renal
3	183.2	16.2	1663	24	ABK63719	Rat sequence diffe
4	173.6	15.3	1580	24	ABN95678	Gene #2176 used to
5	118.8	10.5	1413	23	AAS64762	DNA encoding novel
6	86.2	7.6	729	24	AAD33699	Human secreted pro
7	76.6	6.8	1824	23	AAS64761	DNA encoding novel
8	67.6	6.0	972	22	AAH67519	C glutamicum codin
C	67.6	6.0	349980	22	AAH68532	C glutamicum codin

	10	64.4	5.7	1272	21	AAC39644
	11	64.4	5.7	1619	21	AAC49339
	12	64.2	5.7	1431	24	ABL19796
C	13	58.2	5.1	269223	22	AAF28554
	14	57.6	5.1	2141	24	AAD22002
	15	53.6	4.7	1005	22	AAH66357
	16	53.6	4.7	1206	21	AAC47338
	17	53.6	4.7	1459	21	AAC37731
	18	53.6	4.7	349980	22	AAH68520
C	19	46	4.1	30078	21	AAH61520
C	20	46	4.1	349980	21	AAF21608
C	21	46	4.1	1437668	21	AAH81490
C	22	44.6	3.9	197	22	AAK24363
C	23	44.6	3.9	600	22	AAK11852
C	24	44.6	3.9	1365	23	ABL15847
C	25	44.6	3.9	2787	23	ABL15846
	26	44	3.9	1431	23	ABL28159
	27	44	3.9	3792	23	ABL28158
	28	43.2	3.8	1425	21	AAH75154
	29	43.2	3.8	1425	21	AAH75173
	30	43.2	3.8	1425	21	AAH75174
	31	42.6	3.8	912	24	ABK79532
	32	41.6	3.7	1425	21	AAH75172
C	33	39	3.4	5403	20	AAH64140
C	34	38.6	3.4	630	21	AAF08640
C	35	37.8	3.3	65	24	ABN53881
C	36	37	3.3	249	21	AACT0024
C	37	36.8	3.2	3295	24	ABK49478
C	38	36	3.2	396	21	AAH30900
C	39	36	3.2	5007	22	AAK52839
C	40	35.8	3.2	2520	23	AAS59595
C	41	35.6	3.1	173	21	AACT1209
C	42	35.4	3.1	945	23	ABV24385
C	43	35.4	3.1	1141	22	AAH57369
C	44	35.4	3.1	1149	24	ABN6877
C	45	35	3.1	1749	23	ABL14371

ALIGNMENTS

RESULT 1	AAO91108	standard; cDNA; 2263 BP.
ID	AAO91108	
AC	AAO91108;	
DT	17-DEC-1995	(first entry)
DE	Hamster ileal/renal bile acid cotransporter.	
KW	Ileal/renal bile acid cotransporter; therapeutic; gene therapy;	
KW	diagnostic; ss.	
OS	Cricetulus griseus.	
FT	Key	Location/Qualifiers
FT	CDS	109..1152
FT		/*tag= a
PN	W09517905-A1.	
PD	06-JUL-1995.	
PF	29-DEC-1994;	94WO-US14431.
PR	29-DEC-1993;	93US-0176126.
PA	(UTWA-) UNIV WAKE FOREST.	
PI	Dawson PA;	
DR	WPI, 1995-246189/32.	

Arabidopsis thalia
Arabidopsis thalia
Human NS cDNA sequ
Genomic fragment #
Human transporters
C glutaminc codin
Arabidopsis thalia
Arabidopsis thalia
C glutaminc codin
N. meningitidis pa
Neisseria meningit
N. meningitidis B
Human brain expres
Human brain expres
Drosophila melanog
Drosophila melanog
Drosophila melanog
CDNA encoding a mu
CDNA clone encodin
CDNA clone encodin
Bacillus clausii g
CDNA clone encodin
Mouse prothrombina
Fusarium venenatum
Mouse spliced tran
Human secreted pro
DNA encoding OSF-2
Human colon cancer
Human polynucleoti
Protonbacterium
Human secreted pro
Human prostate exp
Human heart cell s
Gene #3375 used to
Drosophila melanog.

DR P-PSDB; AAR77224.

Hamster and human ileal and bile acid transport. DNA and protein -
useful in treatment of e.g. hypercholesterolaemia, diabetes and
various digestive diseases, and in gene therapy to restore bile acid
uptake activity.

PS Claim 4; Page 98-103; 148pp; English.

The ileal/renal bile acid cotransporter cDNA is cloned in an expression vector (plasmid pCMX or plasmid pCMV5) under the control of a baculovirus Autographa californica nuclear-polyhedrosis virus gene promoter. The cytomegalo virus immediate early gene promoter, the SV40 virus late gene promoter or an inducible promoter e.g. the laclose operon promoter, and expressed in CHO, MDCK, Caco2, BHK or preferably COS-1A cells. The cotransporter is useful in the treatment of hypercholesterolaemia, diabetes, heart disease, liver disease and various digestive disorders. The cDNA may be used in gene therapy to restore bile acid uptake activity to patients whose ileum has been surgically resected for diseases such as Crohn disease, patients born with congenital defects in the bile transporter, and patients suffering from adult-onset chronic idiopathic bile acid diarrhoea. The DNA and protein may be used in screening methods as modulators of ileal/renal bile acid cotransport activity. The DNA can also be used to detect mutations and RFLPs in human ileal/renal bile acid cotransporter genes by amplification with primers (see AAQ91110-15).

SQ Sequence 2263 BP; 672 A; 451 C; 476 G; 664 T; 0 other;

Query Match	Score	DB	Length
28.3%	320.4	16	2263

Matches 522; Conservative 0; Mismatches 336

Matches 522; Conservative 0; Mismatches 336; Indels 0; Gaps 0.

OY	80	ATGGAACCTGGAGCTCGCTTTTCACAGTGGTGTCCACTGGAGATAGGGGCTCTCATGT	139
Db	188	AGCCCATCTTCAGCGGTGGATGAGACCGTGTCAACATCTCTTAAGCTTGTAATGT	247
OY	140	TCTCTTTGGAGTGTCCGTGGAGATCCGGAAGCTGTGTGTGCAACATCAGAGAACCTGTGG	199
Db	248	TTTTCATGGGGGTGCATATGTGAACCTCACAAAGTTTCTGGGACACCTTAAGCGGCATGTGG	307
OY	200	GGATTGCTGTGGGACCTGCTCTGCAATTTTGGGCTCATGCTTTTAACGCTTATCTCTGG	255
Db	308	GGATGCTGTGGGCTCTCTCTGTGCATTTGGAAATCATGCTCTTCACAGGTTTGCTCTGT	367
OY	260	CCATTAGCTTTTCTCGAAGCCAGTCCAAAGCTATGCTGTTCATCATGGGCTGTGCC	318
Db	368	CCGTGGCTTTTGGCATCTCCACAGTCAAGCTGTGTGTGTGTGATTCACAGGTTTGTCTGCC	427
OY	330	CGGGGGGCAACATCTCTTAACATTTTCACTTCTGGGTGAATGAGATATGAGATCTCAGCA	379
Db	428	CTGGAGGAATGCTCTCAATATCTTAAGCCATTTGGGTAAGATGGAGCATGGAACCTCAGCG	487
OY	380	TGAGTATGCAACCTGTTCACCGTGGCCGCCCTGGGAATGATGCCACTGTGCATTTATC	439
Db	488	TTAGCATGCAACCTGCTCCACCGCTCTTGCCCTTGGAAATGAGCCCTTGTGCTCTTCA	547
OY	440	TCTAACCCGTGCTGAGAGTCTTCAAGAGATGTCAACATCTCTTATCAGAACATAGAA	499
Db	548	TCTAATACCAAGATGTGGGTGACTCAGGGAGCATTTGTGATTCCTTAATGACAGCATTTGGCA	607
OY	500	TTACCTGTGTGCTCTGACCATTCCTGTGGCTTTTGGTGTCTATGTGAATTACAGATGAGC	558
Db	608	CTTCTCTGTGTGCTCTGTATTATTCGTGTTCCATTTGGAATGTAATGTAAATCACAAAATGGC	666
OY	560	CAAAACATTCAAAAATCATTTCTCAAGATTGGGCGCTGTGTGGGGGTCTCTCCTCTGG	619
Db	668	CCCAAAAACAAAGATCATATCTTAAATTTGATTCATCCGAGGTGCATTTCTCATTTGTTTC	727
OY	620	TGCTGGCAATGTCTGTGTGTGTCTGTGGCCAAAGAGATCTTGGAAATCAGACATCAACCTTTC	679
Db	728	TGATGCTGTGTGTGGAGAAATATCTATCCAAAGTGTCTGGACCATTTGAACCAAGCTGT	787

Qy	680	TGACCATAGTTTCATCTTTCTTTGATTGGCAATGACGGGTTTTCTGCTGGACATT	739
Db	788	GGATTATAGAACCATATATCTTATAGCTGGCTACGGGCTTTTCTCGGGTAGAA	847
Qy	740	TTAACCCACCACTCTTGCGCAAGGTGCAGGACAAATTTCTTTAGAACTGAGCTCAGATA	799
Db	848	TTGCTGTGTCAACCTGTGTACAGGGTCCCAACAGTTGCTTTGGAAACCGGGTTGCAGAAC	907
Qy	800	TTCAAGATGTGATCAACCATGTCTCCAGTATCTTTTCACATGCTGTAGACTTGGTCCAGATGT	859
Db	908	CTCAGCTGTGTCCACCATTTGTGTGACGTTTCTTTCAGCCCTGTAGAACCTCAACCTTGTGT	967
Qy	860	TGAGTTTCCACTGTGGCTTATGGAATCTTTCCAGCTGATAGATGATTTCTTATTTGTGAC	919
Db	968	TCACCTTCCCTCATCTACAGCAATCTTCCAGATGCGCTTTCAGCAATATCATTTAGGAG	1027
Qy	920	CATATCAGACGTACAGA	937
Db	1028	CTTATGTGCATACAGAA	1045

RESULT 2

AAQ91105
TD 780

ID	AAQ91109	standard; cDNA; 1047 BP.

AC AAQ91109;

DT 17-DEC-1995 (first entry)

DE Human ileal/renal bile acid cotransporter

KW ileal bile acid cotransporter; therapeutic; gene therapy;

KW diagnostic; ss.

OS Homo sapiens.

FH Key

PT

PN W09517905-A1

PD 06-JUL-1995.

PF 29-DEC-1994;

PR 29-DEC-1993;

PA (UYWA-) UNIV

PI Dawson PA;

DR WPI; 1995-240

2000

PT useful in tre

PT uptake activity:

PS Claim 5; Page 11

CC The ideal/re

CC of a baculo

CC the .SV40 vir

CC preferably Co

CC disease and v

PT Hanesite and human ileal and bile acid transport DNA and protein -
 PT useful in treatment of e.g. hypercholesterolemia, diabetes and
 PT various digestive diseases, and in gene therapy to restore bile acid
 PT uptake activity.
 XX
 PS
 PS Claim 5; Page 107-111; 148pp; English.
 XX
 CC The ileal/renal bile acid cotransporter cDNA is cloned in an
 CC expression vector (plasmid pCMX or plasmid pCMV5) under the control
 CC of a Bacillo virus Autographa californica nuclear-polyhedrosis virus
 CC gene promoter, the cytomegalio virus immediate early gene promoter,
 CC the SV40 virus late gene promoter or an inducible promoter e.g. the
 CC lactose operon promoter, and expressed in CHO, MDCK, CaCo2, BHK or
 CC preferably COS-1a cells. The cotransporter is useful in the
 CC treatment of hypercholesterolemia, diabetes, heart disease, liver
 CC disease and various digestive disorders. The cDNA may be used in
 CC gene therapy to restore bile acid uptake activity to patients whose

CC sample that has been exposed to a compound or agent. Hepatotoxicity
CC is characterized by centrilobular necrosis and steatosis. The present
CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
CC which is differentially expressed in response to a hepatotoxic agent.
XX
XX

SO Sequence 1663 BP; 450 A; 460 C; 325 G; 428 T; 0 other;

Query Match 16.2%; Score 183.2; DB 24; Length 1663;
Best Local Similarity 53.6%; Pred. No. 8.9e-47;
Matches 430; Conservative 0; Mismatches 363; Indels 9; Gaps 2;

QY 119 TGATGATGAGGCGCTCATGTTCTTTGGAGATCCGCGAGATCCGAGCTGTGT 178
DB 219 TATGTTGCTTATATCATGCTCTCACTGGGTCGACCATGATTCAGATCAAG 278
QY 179 CGCATATCAGAGAGCCCTGGGCGATTCGTGGGAGCTGCTCCAGTTTGGGCTCATGC 238
DB 279 CTCACCTTGGAGAGCCCAAGGGGTATGCTTGGTGGCCAGTTTGGCATCATGC 338
QY 239 CTTTACAGCTTATCTCTGGCCATTAGCTTTTCTCTGAAGCCAGTCCAACTATTGCTG 298
DB 339 CCTCGCTCTTTCTTCTCGGCAAGATCTTTCACCTGAGCAATTTGAAGCTTGGCCA 398
QY 299 TTCTCATGATGGGCTGCTGCGGGGGGACCATCTCTAATTTTCACTTCTGGGTTG 358
DB 399 TCTCATCTGTGGCTCTCTCCGGGGGAACTTGTCAACCTTTCACCTTGGCCATGA 458
QY 359 ATGAGATATGATCTCAGCATCATGATGACAACCTGTTCCACCGTGGCCCTGGGAA 418
DB 459 AGGGGACATGAACCTCAGCATGTGATGACCACTGCTCCAGTTCAGTCCCTTGGGA 518
QY 419 TGATGCTCTGCTGATTTATCTCTAACC--TGCTCTGAGTCTTTCAGCAGATTTCA 475
DB 519 TGATGCTCTGCTGATTTATGTTTACAGAAAGGATCTCAAGATGAGACCTTAAAGACA 578
QY 476 CCATTCCTATACGAACATGAAATTAACCTGTGTGCGCCGACATTTCTGTTGGCTTGG 535
DB 579 AGGTGCTCTCAAAAGGATATGATATCACTATGCTCAATGTTCTCATTTCTTGACATATG 638
QY 536 GTGTCTATGATGATTCAGATGAGCCAAACATCAATTCATTTCAAGATTTGGGCGG 595
DB 639 GGATGCTCTCAAGTCCAAAGGCCACATATGATACCTTCAACCTTCAAGGAGGATGA 698
QY 596 TTGTTGGTGGGCTCTCTCTTGTGTGTGTCAGTCTGTGTGTGTGTGTGTGTGTGTGT 655
DB 699 TCATCACTTCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 758
QY 656 CTTGGAATTCAGATCATCAC-----CCTTCTGACCATTCAGTTTCATCTTCTTGATTG 709
DB 759 GCATCATGTTCTGATGACACACACTTACTGTGCTACCTCTCTGATGACCTTCTGTG 818
QY 710 GCCATGTCAGGGTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 769
DB 819 GCTTCTGATGGTTTCACTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 878
QY 770 CAATTTCTTGAACCTGAGCTCAGATATTCAGATGTGATCAACATGCTTCAATTTAT 829
DB 879 CCATTCAGATGAGAAAGGATTCACAAACATTCATCTGTGTGTGTGTGTGTGTGTGTGT 938
QY 830 CTTTCTGCTGTGAGCTGT 889
DB 939 CTTTCTGCTGTGAGCTGT 998
QY 890 AGCTGATGATGATTTCTTAT 911
DB 999 AGCTTGCAGAGGATTTCTCAT 1020

RESULT 4
ABN95678 standard; DNA; 1580 BP.
XX
XX
AC ABN95678;

XX 13-AUG-2002 (first entry)
DT Gene #2176 used to diagnose liver cancer.
XX
DB
XX Gene, liver cancer; ds, hepatocellular carcinoma; hepatotropic;
KW metastatic liver tumour; cytostatic; expression profile; disease state;
KW disease progression; drug toxicity; drug efficacy; drug metabolism.
OS Homo sapiens.
XX
XX MO200229103-A2.
PN 11-APR-2002.
PD 02-OCT-2001; 2001WO-US30589.
PF 02-OCT-2000; 2000US-237054P.
PR (GENE-) GENE LOGIC INC.
PA Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
PI MPI; 2002-426119/45.
DR
XX
XX Diagnosing and detecting the progression of liver cancer,
PT hepatocellular carcinoma or metastatic liver tumor in a patient,
PT involves detecting the level of expression of two or more genes in a
XX liver tissue sample
XX
PS Claim 1; SEQ ID NO 2176; 298bp; English.
XX
XX The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumor in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SO Sequence 1580 BP; 400 A; 434 C; 341 G; 405 T; 0 other;

Query Match 15.3%; Score 173.6; DB 24; Length 1580;
Best Local Similarity 51.9%; Pred. No. 9.2e-44;
Matches 445; Conservative 0; Mismatches 404; Indels 9; Gaps 2;

QY 119 TGATGATGAGGCGCTCATGTTCTTTGGAGATCCGCGAGATCCGAGCTGTGT 178
DB 180 TATGTTGCTTATATCATGCTCTCACTGGGTCGACCATGATTCAGATCAAG 239
QY 179 CGCATATCAGAGAGCCCTGGGCGATTCGTGGGAGCTGCTCCAGTTTGGGCTCATGC 238
DB 240 CTCACCTTGGAGAGCCCAAGGGGTATGCTTGGTGGCCAGTTTGGCATCATGC 299
QY 239 CTTTACAGCTTATCTCTGGCCATTAGCTTTTCTCTGAAGCCAGTCCAACTATTGCTG 298
DB 300 CCTCAGCGCTTGT 359
QY 299 TTCTCATGATGGGCTGCTGCGGGGGGACCATCTCTAATTTTCACTTCTGGGTTG 358
DB 360 TCTTGT 419
QY 359 ATGAGATATGATCTCAGCATCATGATGACAACCTGTTCCACCGTGGCCCTGGGAA 418
DB 420 AGGGGACATGAACCTCAGCATGTGATGACCACTGCTCCACCTTGTGTGCTTGGGA 479

Oy		419	TGAAGCCACTCGCATTTTATCTTGACACC---TGGTCCTGAGAGTCTTCAGAGAATCTCA	475
Dd		480	TGAATCCTCTCTCTCTGTACATCTACTCCAGGGGAAATTATGATGAGGAGCTTGANAGCA	539
Oy		476	CCATTCTTATCAGAACATAGAAATTAACCTGTGTGTGCCTGACCAATTCCTGTGGCCTTTG	535
Dd		540	AGTGAGCCCTATAAAGGCAATCGATATATCATCTGTCTGTGATTCCTTGACCATATG	599
Oy		536	GTCGTCTATGTGAATTAACGATGAGGCCAAAACAATCCAATAATCTTCAAGATTGGGGCCG	595
Dd		600	GGATCTGTCCTCAAAATCCAAAGCGGCACAAATACATGCGCTATGTATCAAGAGGAGGATGA	659
Oy		596	TTGTTGGTAGGGGTCTCTCCCTCGTGNGATGCGAGTGTGCTGTGTGGTCCCTGGAGAAAGAT	655
Dd		660	TCAATCATTTCTCTTGTGCAAGTGTGCCCCGTACAGATTCTCTGTGCCATCAATGTGGGGAAGA	719
Oy		656	CTTGGAAATCAGACATCAC-----CCTTCTGACCATCAAGTTTCAATCTTTCCTTTGATTG	709
Dd		720	GCATCATGTTGGCCATGACACCACTCTTGATTTGCCACCTCCCTGANTGCTTTTATTTG	779
Oy		710	GCATATGTACAGGGTTTTCTGTGTGGACATTTTAAACCACAGCTTTGGCAAAGGTGCAGA	769
Dd		780	GCTTCTCTCTGGGTATGTCTCTGTGCTCTCTTGTGCTCAATGAGAGGTGCACAGCA	839
Oy		770	CAATTCTCTTGAACCTGAGCTCAGAAATTAATCAGATGNCATCCAGTCTCCAGTTAT	829
Dd		840	CTGTATAGATGAGAGCTGATGATGCCAAATATGTCACACTCTGTTCCACCATCTTCAATGTGG	899
Oy		830	CTTTCACGTCTGAGCACTTGTGTCCAGATGTTGAGTTTCCCACTGGCCTATGAGACTCTTCC	889
Dd		900	CCTTTCACACTGAAAGTCAATGTGAGCACATTTTCTTTCCTTCCCCTCTTAATGATTTTCC	959
Oy		890	AGCTATATGATGAGATTTCTTATTTGTGCAGCATATCAGACGTACAGAGAGATTTGAAGA	949
Dd		960	AGCTTGGAGAAAGGGCTTCTCTCCATTTGCCATATTTTGTGTATGAGAAATTCAGACTTC	1019
Oy		950	ACAAACATGAAAAAAGA	967
Dd		1020	CCAGGATTAACCAAAAA	1037
<hr/>				
RESULT 5				
AAS64762				
ID	AAS64762	standard; cDNA; 1413 BP.		
XX	AAS64762;			
<hr/>				
XX	13-FEB-2002	(first entry)		
DE	DNA encoding novel human diagnostic protein #566.			
XX				
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;			
KW	food supplement; medical imaging; diagnostic; genetic disorder; ss.			
OS	Homo sapiens.			
XX				
PN	WO200175067-A2.			
XX				
PD	11-OCT-2001.			
XX				
PF	30-MAR-2001; 2001WO-US08631.			
XX				
PR	31-MAR-2000; 2000US-0540217.			
FR	23-AUG-2000; 2000US-0649167.			
XX				
PA	(HYSE-) HYSEQ INC.			
XX				
PI	Drimanac RT, Liu C, Tang YT;			
DR	WPI, 2001-639362/73.			
DR	P-PsDB; ABG00575.			
XX				

PT	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity -
PS	Claim 1, SEQ ID No 566, 103bp, English.
XX	
CC	The invention relates to isolated polynucleotide (I) and
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC	and gene mapping, and in recombinant production of (II). The
CC	polynucleotides are also used in diagnostics as expressed sequence tags
CC	for identifying expressed genes. (II) is useful in gene therapy techniques
CC	to restore normal activity of (I) or to treat disease states involving
CC	(II). (II) is useful for generating antibodies against it, detecting or
CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II). (I) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.
CC	The polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. AAS6197-AAS94564 represent novel human
CC	diagnostic coding sequences of the invention.
CC	Note: The sequence data for this patent did not appear in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	
SEQ	Sequence 1413 BP; 374 A; 334 C; 345 G; 360 T; 0 other;
Query Match	10.5%; Score 118.8; DB 23; Length 1413;
Best Local Similarity	62.4%; Pred. No. 1.7e-26;
Matches 186; Conservative	0; Mismatches 112; Indels 0; Gaps 0;
QY	80 ATGGAACCTGGAGCTGTTTACACAGTGGTGCACGTGATGAGGCGCTGTCAGT 139
DB	863 ATAAACCTCCTAAGTGTGCTCTTAAGTACGGGTGACCATCTGTGGCTTGGAAGT 922
QY	140 TCTCTTTGGAGATGTTCCGTGAGATCCGGAAGCTGTGGTCGACATCAGAGACCTTGGG 199
DB	923 TCTCCATGAGATGACAGCTGGAATCAAGAAATTTTAAAGGCACTAAGCGGCGGTGG 982
QY	200 GCATTGCTGTGGAGCTGCTCCAGATTGGGCTCATGCTTTTACAGCTTATCTCTGG 259
DB	983 GCATTGTGTGGCTCTCTGTGAGATTGGAATCATCCCTCCACAGAGATTCACTCTGT 10424
QY	260 CCATTAGCTTTCTCTGAGGCACTCCAGTATATGCTGTCTATCATGTGGGCTGTGCC 319
DB	1043 CGGTGGCTTTGAGATCTCTCCGCTCCAGGCGCGTGAAGTCTCATTAAGATGCTGCC 11024
QY	320 CGGGGGGACACATGCTTAACTTTTACACCTTCTGGGTTGAGAGATATGATCTCAG 377
DB	1103 CTGAGGAGACTCCTCCATATCTTGGCTTATGGGTGATGCGACATGAGACTTGAG 1160
RESULT 6	
AAD33699	
ID	AAD33699 standard; cDNA; 729 BP.
XX	
AC	AAD33699;
XX	
DT	01-JUL-2002 (first entry)
XX	
DE	Human secreted protein-encoding gene 8 cDNA clone HBCPB32, SEQ ID NO:18.
XX	
KW	Human; secreted protein; immune disorder; antiallergic; anti rheumatic;
KW	rheumatoid arthritis; breast neoplasia; breast cancer; antiarthritis;
KW	neurological disease; Alzheimer's disease; Parkinson's disease; trauma;
KW	Tourette syndrome; encephalitis; cystostatic; haemostatic; anaemia; mania;
KW	antiinflammatory; ophthalmological; dermatological; immunostimulatory;
KW	immunomodulatory; immunosuppressive; antibacterial; antiparasitic;
KW	gene therapy; autoimmune disease; Huntington's disease; meningitis;

demyelinating disease; peripheral neuropathy; congenital malformation;
 spinal cord injury; peripheral neuropathy; ischaemia; perception;
 multiple sclerosis; infarction; haemorrhage; schizophrenia; dementia;
 depression; panic disorder; learning disability; ALS; feeding disorder;
 hyperproliferative disorder; sleep pattern; cardiovascular disorder;
 reproductive disorder; digestive system disorder; behavioural disorder;
 gene; ss.
 Homo sapiens.
 Key CDS Location/Qualifiers
 89..679
 /tag= a
 /product= "Human secreted protein"
 /transl_except= (pos:599..601, aa:Xaa)
 /transl_except= (pos:611..613, aa:Xaa)
 /transl_except= (pos:617..619, aa:Xaa)
 /transl_except= (pos:629..631, aa:Xaa)
 /transl_except= (pos:641..643, aa:Xaa)
 /transl_except= (pos:650..652, aa:Xaa)
 /transl_except= (pos:653..655, aa:Xaa)
 /note= "Xaa equals any of the naturally occurring
 L-amino acids"
 89..199
 /tag= b
 200..676
 /tag= c
 /product= "Human mature secreted protein"
 sig_peptide
 mat_peptide
 WO200216390-A1.
 28-FEB-2002.
 17-JAN-2001; 2001WO-US01435.
 18-AUG-2000; 2000US-226282P.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;
 Moore PA, Wei P, Edner R, Duan DR, Shi Y, Choi GH, Fischella M;
 Ni J;
 WPI; 2002-304113/34.
 P-PSDB; AAE21198.
 An isolated nucleic acid molecule (1) comprising a polynucleotide which
 encodes a polypeptide useful in the diagnosis and treatment of
 disorders e.g. immune disorders -
 Claim 1; Page 445; 534pp; English.
 AAD33692-AAD33736 represent cDNAs corresponding to 21 human secreted
 protein genes, and AAE21191-AAE21235 represent the proteins they encode.
 AAE21236-AAE21280 represent human secreted protein fragments. The genes
 and their corresponding secreted proteins are useful for preventing,
 treating or ameliorating medical conditions, e.g., by protein or gene
 therapy. Pathological conditions can be diagnosed by determining the
 amount of the new protein in a sample or by determining the presence of
 mutations in the new genes. Specific uses are described for each of the
 21 genes, based on the tissues in which they are most highly expressed,
 and include developing products for the diagnosis or treatment of
 immune or autoimmune diseases e.g. AIDS (acquired immune deficiency
 syndrome), asthma, anaemia and rheumatoid arthritis, breast neoplasia
 and breast cancer, neurological diseases e.g. Alzheimer's disease,
 Parkinson's disease, Huntington's disease, Tourette syndrome,
 meningitis, demyelinating disease, peripheral neuropathies, neoplasia,
 trauma, congenital malformations, spinal cord injuries, toxic
 neuropathies induced by neurotoxins, peripheral neuropathies, multiple
 sclerosis, ischaemia and infarction, haemorrhages, schizophrenia, mania,
 dementia, depression, panic disorder, learning disabilities, ALS,
 altered behaviour e.g. disorders in feeding, sleep patterns, balance
 and perception, encephalitis, disorders in cardiovascular, neural/

sensory, reproductive and digestive systems, behavioural disorders and
 hyperproliferative disorder. The present sequence represents a human
 secreted protein-encoding cDNA of the invention.
 SQ Sequence 729 BP; 148 A; 190 C; 169 G; 210 T; 12 other;
 Query Match 7.6%; Score 86.2; DB 24; Length 729;
 Best Local Similarity 49.0%; Pred. No. 2.2e-16;
 Matches 352; Conservative 9; Mismatches 339; Indels 19; Gaps 5;
 256 CTGGCCATTAGCTTCTCTGAAGCCAGTCCAGGTAATGCTGCTCATCATGAGGCTGC 315
 2 CTGGCCCTCGCTCTTAAGTGAAGAGGAGGCGCGGCTCTCTGCTGCTGC 61
 316 TGCCCGGGGGGACCATCTCAACATTTTCACTTCTGCGTTGATGAGATATGATCTC 375
 62 TGTCGGCGGGAATCTCTCAATCTTATGTCCTGCTGTTAGCGGAGCATGAACCTC 121
 376 AGCATCATATGACAACTGTTCCACCGTGGCGCGCTGGGAATGATGCCACTGCAAT 435
 122 AGCATCATATGACAACTGTTCCACCGTGGCGCGCTGGGAATGATGCCACTGCAAT 181
 436 TATCTCTACCTGCTGCTGAGTCTTCAAGAGATCTCACCATCTTATC---AGAA 491
 182 TGATCTTACAGCTGAGCTTGA-TCACACCCCTATCTGACATTAACCCCTAGGAC 240
 492 CATAGAAATTAACCTTGTGTGCTGACCAATTCCTGTGCTTGTATGTAATTA 551
 241 CGTACCCCTGACTCTCTGACAGACTCATATCTATCGGTTGGGCTTCAATTCGCTA 300
 552 CAGATGGCCAAACATCAAAATATCTCAAGTTGGGCGCTTGTGTGCTGCTCCT 611
 301 CAATACAGCGGGGTGCTGACTATGTAAGTT--TCCTGTGCTCTGCTAGT 357-
 612 CTTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 671
 358 GACTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 417
 672 CACCTTGTGACCACTGCTTCA-----TCTTCTTGTATGCTGCTGCTGCTGCT 722
 418 TATCCCTGAGCTGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 477
 723 TTTCTGCTGCTGCTTTCACCACTCTTGGGAAGTGGAGAGATTTCTTGA 782
 478 TTATGTTAGTACTCTCTTCACTTTCACCACTGCAAGAGAGAGAGAGAGAGAGAG 537
 783 AACTGAGCTGAGATATTCAGATGTCATGATGTCATGTCATGTCATGTCATGTCAT 842
 538 AACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 595
 843 GCATTTGTCAGATGTTGAGTTCCACCTGAGCTTCCAGCTGATGATGATG 902
 596 ATTATGAG 655
 903 ATTCTTATGTTGAGATATGATGATGATGATGATGATGATGATGATGATGATGAT 961
 656 GGGATTTTGTATTAATTAATAAAGTATGATGATGATGATGATGATGATGATGAT 714
 RESULT 7
 ID AAS64761 standard; cDNA; 1824 BP.
 AC AAS64761;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #565.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
 OS Homo sapiens.

XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX P-PSDB; ABG00574.
XX

PT New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -

PS Claim 1; SEQ ID No 565; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AA564197-AA594564 represent novel human
XX diagnostic coding sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1824 BP; 409 A; 477 C; 486 G; 452 T; 0 other;

XX Query Match 6.8%; Score 76.6; DB 23; Length 1824;
XX Best Local Similarity 58.6%; Pred. No. 4,1e-13;
XX Matches 133; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 80 ATGAAACCTGGAGCTGTTTACAGTGTGTCCACTGTGTATGATGGGCTGCTCATGT 139
DB 80 ATAACATCTTAAGTGTGTGCTTAAGTACGTGTCTACCATCTGTGTGCTTGTGATGT 139
QY 140 TCTCTTGGAGATGTCGCGAGATCCGAGACCTGTGTGCGACATTCAGAGAACCTCTGG 199
DB 140 TCTCATATGGAGTCAACGTCGAAATCAAGAAATTTCTAAGGGCAATAAAGCGCGTGGG 199
QY 200 GCATTGTGTGGAGTGTGCTGCTCCAGTTTGGGCTCATGCTTTTACGTTATCTCTGG 259
DB 200 GCATTGTGTGGTCTTCTCTGTCTGATTTGGAATATGCCCCCTCAGAGATTTCATCTGT 259
QY 260 CCATTAGCTTTTCTCTGAAGCCAGTCCAGAGCTATTGCTGTCTCATC 306
DB 260 CGGTGCTTTGACATCTCCGCTCCAGCGCGTGTAGTAACCTATTC 306

RESULT 8
AAH67519
ID AAH67519 standard; DNA; 972 BP.
XX

AC AAH67519;
XX
XX 26-SEP-2001 (first entry)
DT
XX
XX C glutamicum coding sequence fragment SEQ ID NO: 2554.
DE
XX
XX Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW organic acid synthesis; ds.
XX
XX Corynebacterium glutamicum.
OS

XX EP1108790-A2.
XX
XX 20-JUN-2001.
XX
XX
XX
XX

XX 18-DEC-2000; 2000EP-0127688.
XX
XX
XX

XX 16-DEC-1999; 99JP-0377484.
XX
XX 07-APR-2000; 2000JP-0159162.
XX
XX 03-AUG-2000; 2000JP-0280988.
XX

XX (KYOW) KYOWA HAKKO KOGYO KK.
XX

XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
XX Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX

XX WPI; 2001-376931/40.
XX
XX P-PSDB; AAG92300.
XX

XX Novel polynucleotides derived from Coryneform bacteria, for identifying
XX mutation point of a gene, measuring expression of a gene, analysing
XX expression profile or pattern of a gene and identifying homologous gene
XX

XX Claim 8; SEQ ID NO: 2554; 246bp + Sequence Listing; English.

XX The present invention provides a number of nucleotide and protein
XX sequences from the Coryneform bacterium Corynebacterium glutamicum. These
XX are useful for identifying the mutation point of a gene derived from a
XX mutant of coryneform bacterium, measuring expression amount and
XX analysing the expression profile or expression pattern of a gene derived
XX from Coryneform bacterium, and identifying a homologue of a gene derived
XX from coryneform bacterium. Coryneform bacteria are useful for producing
XX amino acids, nucleic acids, vitamins, saccharides and organic acids,
XX particularly L-lysine. The present sequence is a nucleic acid described
XX in the exemplification of the invention.

XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from the
XX European Patent Office.

XX Sequence 972 BP; 198 A; 274 C; 241 G; 259 T; 0 other;

XX Query Match 6.0%; Score 67.6; DB 22; Length 972;
XX Best Local Similarity 51.3%; Pred. No. 2e-10;
XX Matches 157; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY 129 GCTGTCACTTTCTTTTGGATGTCCGTGGAATCCGAGACGTGTGTGCATCATG 188
DB 141 GATATCATATGTTTCAACATGAGGTTTGAACCTTACCGGTGCCGATTTTCAGATGTGCTTAA 200

QY 189 GAGACCCGCGGAGCATATGCTGTGGAGACTGCTGCGCAGTTTGGGCTCATGCTTTTACAGC 248
DB 201 ACGTCACTGCTATCTTGATCGGTGATGAGCGCAGTTTGTTCATATGCTTCATCTGCGC 260

QY 249 TTATCTCTGCGCATATGACTTTTCTGAGCCAGTCACAGCTATGCTGTCTTCATCAT 308
DB 261 GATGTGTGTGCGAAATGTTCAACCTCAACCCAGCACTCCCGTGTGCTTTCATATGCT 320

QY 309 GGGCTGTGCGCGCGGCGGAGCAATCTTAATATTTTCACTTCTGCGGTGATGAGAGAT 368
DB 321 GGGATCGTTCGGGTGCGCACTCTCCAAATGATATGCGTTTCTCGCCGAGGAGATGT 380

QY 369 GGATCTCAGCATAGTATGACAACTGTTCACCGGTGCGCGCTGGGATGATGCCACT 428

DB 381 CCGCTATGCTGATCACCATGACCTCTGTGTGTCACCATTTGTTCCCATCATGACGCTTT 440
QY 429 CTGCAT 434
DB 441 CCTCAT 446

RESULT 9

AAH6532/c
ID AAH6532 standard; DNA; 349980 BP.

AC AAH6532;

DT 26-SEP-2001 (first entry)

DE C glutamicum coding sequence fragment SEQ ID NO: 7067.

XX Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KM organic acid synthesis; ds.

XX Corynebacterium glutamicum.

PN EP108790-A2.

PD 20-JUN-2001.

PF 18-DEC-2000; 2000EP-0127688.

XX 16-DEC-1999; 99JP-0377484.

PR 07-APR-2000; 2000JP-0159162.

PR 03-AUG-2000; 2000JP-0280988.

XX (KYOM) KYOMA HAKKO KOGYO KK.

XX Nakagawa S, Mizoguchi H, Ando S, Hayaishi M, Ochiai K, Yokoi H;

PI Tateishi N, Senon A, Ikeda M, Ozaki A;

DR WPI; 2001-376931/40.

XX Novel polynucleotides derived from Coryneform bacteria, for identifying

PT mutation point of a gene, measuring expression of a gene, analysing

PT expression profile or pattern of a gene and identifying homologous gene

PT

XX Disclosure; SEQ ID NO: 7067; 246bp + Sequence Listing; English.

XX The present invention provides a number of nucleotide and protein

CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These

CC are useful for identifying the mutation point of a gene derived from a

CC mutant of coryneform bacterium, measuring expression amount and

CC analysing the expression profile or expression pattern of a gene derived

CC from Coryneform bacterium, and identifying a homolog of a gene derived

CC from Coryneform bacterium. Coryneform bacteria are useful for producing

CC amino acids, nucleic acids, vitamins, saccharides and organic acids;

CC particularly L-lysine. The present sequence is a nucleic acid described

CC in the exemplification of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from the

CC European Patent Office.

CC

XX Sequence 349980 BP; 80900 A; 98397 C; 92139 G; 78544 T; 0 other;

Query Match : 6.0%; Score 67.6; DB 22; Length 349980;

Best Local Similarity 51.3%; Pred. No. 6.4e-09;

Matches 157; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY 129 GCTGCTCATGTTCTCTTTGGATGTTCCGTGAGATCCGAAAGCTGTGTCGACATCG 188

DB 66869 GATCATCATGTTCCACCATGAGTGTGACCTTGACGGGCGCCGATTTTCAATGCTGCTTAA 66810

QY 189 GAGACCCCTGGGCGATTCGCTGGGAGCTGCTGCTGCGATTTGGGCTCATGCTTTTACAGC 248

DB 66809 ACGTCCACTGCGCTATCTTGATGCGGTGATGAGCCGATTTGTATCATGACCTTCTGCG 66750
QY 249 TTATCTCCGTGGCCATTAAGCTTTTCTGTGAGCCGATTCAGCTATTTGCTTCATCAT 308
DB 66749 GATCGTGGTTGGGAAATGTTCAACCTTCACCGACGACATCGCCGTTGCGCTTCTATGCT 66690
QY 309 GGGCTGCTGCGCGGGGGGACCATCTTAAACATTTTCACTTTGCGTTGATGAGATAT 368
DB 66689 GCGATCCGTTCCGGGTGGACCTCTCCCAATGTGATTCGTTTCGCGCGAGAGATGT 66630
QY 369 GGATCTCAGCATTCAGTATGACCAACCTTTCCACCGGTGGCGCGCTGGGATGATGCACAT 428
DB 66629 CCGCTATCGGCTACCATTAAGCTCTGTGTCCACATTTGTTCCCAATCATGACGCTTT 66570
QY 429 CTGCAT 434
DB 66569 CCTCAT 66564

RESULT 10

AAC39644
ID AAC39644 standard; DNA; 1272 BP.

AC AAC39644;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 25386.

XX Hybridisation assay; genetic mapping; gene expression control;

KM protein identification; signal transduction pathway;

XX metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

XX EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 29-MAR-1999; 99US-0126264.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0128845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132484.

PR 06-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 06-MAY-1999; 99US-0132487.

PR 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0133256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134321.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.
 PR 27-MAY-1999; 99US-0136392.
 PR 28-MAY-1999; 99US-0136782.
 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137528.
 PR 04-JUN-1999; 99US-0137502.
 PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.
 PR 10-JUN-1999; 99US-0138540.
 PR 10-JUN-1999; 99US-0138847.
 PR 14-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139452.
 PR 16-JUN-1999; 99US-0139453.
 PR 17-JUN-1999; 99US-0139459.
 PR 18-JUN-1999; 99US-0139454.
 PR 18-JUN-1999; 99US-0139455.
 PR 18-JUN-1999; 99US-0139456.
 PR 18-JUN-1999; 99US-0139457.
 PR 18-JUN-1999; 99US-0139458.
 PR 18-JUN-1999; 99US-0139459.
 PR 18-JUN-1999; 99US-0139460.
 PR 18-JUN-1999; 99US-0139461.
 PR 18-JUN-1999; 99US-0139462.
 PR 18-JUN-1999; 99US-0139463.
 PR 18-JUN-1999; 99US-0139750.
 PR 18-JUN-1999; 99US-0139763.
 PR 21-JUN-1999; 99US-0139817.
 PR 22-JUN-1999; 99US-0139899.
 PR 23-JUN-1999; 99US-0140353.
 PR 23-JUN-1999; 99US-0140354.
 PR 24-JUN-1999; 99US-0140695.
 PR 28-JUN-1999; 99US-0140823.
 PR 29-JUN-1999; 99US-0140991.
 PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141842.
 PR 01-JUL-1999; 99US-0142154.
 PR 02-JUL-1999; 99US-0142055.
 PR 06-JUL-1999; 99US-0142390.
 PR 08-JUL-1999; 99US-0142803.
 PR 09-JUL-1999; 99US-0142920.
 PR 12-JUL-1999; 99US-0142977.
 PR 13-JUL-1999; 99US-0143542.
 PR 14-JUL-1999; 99US-0143624.
 PR 15-JUL-1999; 99US-0144005.
 PR 16-JUL-1999; 99US-0144085.
 PR 16-JUL-1999; 99US-0144086.
 PR 19-JUL-1999; 99US-0144325.
 PR 19-JUL-1999; 99US-0144331.
 PR 19-JUL-1999; 99US-0144332.
 PR 19-JUL-1999; 99US-0144333.
 PR 19-JUL-1999; 99US-0144334.
 PR 19-JUL-1999; 99US-0144335.
 PR 20-JUL-1999; 99US-0144352.
 PR 20-JUL-1999; 99US-0144632.
 PR 20-JUL-1999; 99US-0144884.
 PR 21-JUL-1999; 99US-0144814.
 PR 21-JUL-1999; 99US-0145086.
 PR 21-JUL-1999; 99US-0145088.
 PR 22-JUL-1999; 99US-0145085.
 PR 22-JUL-1999; 99US-0145087.
 PR 22-JUL-1999; 99US-0145089.
 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.
 PR 23-JUL-1999; 99US-0145218.
 PR 23-JUL-1999; 99US-0145224.
 PR 26-JUL-1999; 99US-0145276.
 PR 27-JUL-1999; 99US-0145913.
 PR 27-JUL-1999; 99US-0145918.
 PR 28-JUL-1999; 99US-0145919.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 02-AUG-1999; 99US-0146389.

PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155119.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158233.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161922.

QY 122 TGATGGGGCTGCTCATGTTCTTCTTGGATGTTCCGTGAGATCCGAGATGCTGTC 181
 DB 183238 TGCTTGGCATGCTCATGCTTGGCATGGGTTTAACTTGAATTTTGGTGAG 183179
 QY 182 ACATGAGAGACCTTGGGACATGCTGTGGAGCTGCTTCCAGTTTGGGCTCATGCTT 241
 DB 183178 TCACCAAAAACCCCAAGCGGGTGAATTAATGAGTATCTTCAATATGTTGATGACGAG 183119
 QY 242 TTACAGCTATCTCCGTCGACATTAACCTTCTCTGAGCGATCCAGCTATGCTGTC 301
 DB 183118 TCATGCTCTTTTGTGTTGTTCAAGCATTTAGGCTTACCACTGATTTGGCTATCGGTGCA 183059
 QY 302 TCATCATGAGGCTGCTGCTGCGGGGAGGACCATCTCTAATTTTCACTTCTGCTGAGT 361
 DB 183058 TCTTAGTGGCTGCTGCTGCTGCGGACCTCTCAAAATGATATCACTTCTTCTGCGAAG 182999
 QY 362 GAGATATGATCTGACATCACTATGACACCTGTTCCACCGTGGCCGCTTGGGAATGA 421
 DB 182998 GCAATACCGCTTATCACTGCTTGCAGACACTCTCCACACTCTTACGCCCTATTTTGA 182939
 QY 422 TGCCACTGCTGATTTATCTCTACACCTGCTGCTG 456
 DB 182938 CGCCAGCTGATTTATTTATTTATTTGCTCAGCCCAATGG 182904

RESULT 14
 AAD22002 standard; cDNA; 2141 BP.
 ID AAD22002 standard; cDNA; 2141 BP.
 AC AAD22002;
 DT 12-FEB-2002 (first entry)
 DE Human transporters and ion channels (TRICH)-10 cDNA.
 KW Human; transporters and ion channel; TRICH; akinesia; cystic fibrosis;
 KW diabetes mellitus; parkinson's disease; myasthenia gravis; dementia;
 KW cardiac disorder; angina; hypertension; myocarditis; hyperglycaemia;
 KW neurological disorder; Alzheimer's disease; cataract; infertility;
 KW Wilson's disease; schizophrenia; Grave's disease; addison's disease;
 KW Huntington's disease; multiple sclerosis; meningitis; hypotensive;
 KW Cardiac; noctropic; neuroprotective; neuroleptic; ophthalmological;
 KW antithyroid; anticonvulsant; goitre; antiinflammatory; ss.
 OS Homo sapiens.
 XX
 Key Location/Qualifiers
 CDS 69..1544
 /tag= a
 /product= "Human transporters and ion channels
 (TRICH)-10"
 FT
 FT WO200177174-A2.
 XX 18-OCT-2001.
 PD 06-APR-2001; 2001WO-US11206.
 XX 06-APR-2000; 2000US-195595P.
 PR 12-APR-2000; 2000US-196872P.
 PR 20-APR-2000; 2000US-199020P.
 PR 28-APR-2000; 2000US-200552P.
 PR 05-MAY-2000; 2000US-202348P.
 PR 11-MAY-2000; 2000US-203495P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 PI Reddy R, Thornton M, Borowsky ML, Tang YT, Khan FA, Tribouley CM;
 PI Gandhi AR, Yeo MG, Sanjana MS, Baughn WR, Nguyen DB,
 PI Policky JL, Yue H, Selhamer JD, Walla NK, Lal P, Kearney L,
 PI Walsh RT, Lu DM, Lu Y, Greene BD, Raumann BE, Patterson C;
 XX
 DR WPI; 2002-017448/02.

DR P-PSDB; AAE13283.
 XX
 PT Polypeptides of human transporters and ion channels, useful for
 PT diagnosing, treating or preventing disorders of transport,
 PT neurological, muscle, immunological and cell proliferative disorders -
 XX
 PS Claim 5; Page 145-146; 150pp; English.
 XX
 CC The invention relates to human transporters and ion channels (TRICH)
 CC and the polynucleotides encoding them. The composition comprising TRICH
 CC or agonist of TRICH is useful for treating a disease or condition
 CC associated with decreased expression of functional TRICH or condition
 CC associated with overexpression of TRICH respectively. The composition
 CC comprising Ab is useful for diagnosing a condition of disease associated
 CC with expression of TRICH in a subject, where the disorders include a
 CC transport disorder such as akinesia, cystic fibrosis, diabetes mellitus,
 CC parkinson's disease, myasthenia gravis, cardiac disorders associated
 CC with transport e.g. angina, hypertension, myocarditis, neurological
 CC disorders associated with transport e.g. Alzheimer's disease, Wilson's
 CC disease, schizophrenia, cataracts, infertility, hyperglycaemia, Grave's
 CC disease, goitre, addison's disease, Huntington's disease, dementia,
 CC multiple sclerosis, bacterial and viral meningitis. TRICH DNA is useful
 CC for generating a transcript image of a tissue or cell type, which
 CC represents the global pattern of gene expression by a particular tissue
 CC or cell type and for analysing the proteome of a tissue or cell type.
 CC TRICH DNA is used in gene therapy. The present sequence is human
 CC TRICH10 cDNA.
 SQ Sequence 2141 BP; 505 A; 573 C; 505 G; 558 T; 0 other;
 XX
 Query Match 5.1%; Score 57.6; DB 24; Length 2141;
 Best Local Similarity 48.5%; Pred. No. 4.5e-07;
 Matches 288; Conservative 0; Mismatches 289; Indels 17; Gaps 4;
 QY 375 CAGATCATGATGACCACTGTTCCACCGGCGCCCTGGGAATGATCCACTCTGAT 434
 DB 818 CAGATCATGATGACCACTGTTCCACCGGCGCCCTGGGAATGATCCACTCTGAT 877-
 QY 435 TTATCTCAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 490
 DB 878 GTGATCTACAGCTGGGCTTGA-TCAACACCCCTATGTCAGTATTAACCCCTAGGA 936
 QY 491 ACATGGAATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550
 DB 937 CCGTACCCCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 996
 QY 551 ACAATGACGCGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 610
 DB 997 ACAATGACGCGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1053
 QY 611 TCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 670
 DB 1054 TGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1113
 QY 671 TCACCTTCTGACCATCAGTTTCA-----TCTTCTTGTGATGGCCATGTCAGG 721
 DB 1114 GTATCTCTGACAGCTGTTATGATGATGATGATGATGATGATGATGATGAT 1173
 QY 722 GTTTCCTGCTGCACTTTTATCCCAAGCTTGGCAAGGAGAGCAATTTCTTAG 781
 DB 1174 GTTATGTTTGAAGTACTCTTTCATCTTCCACCAATGCAAGAGGAGCTATGTCGG 1233
 QY 782 AAATGAGCTCAAAATTTGATGATGATGATGATGATGATGATGATGATGAT 841
 DB 1234 AAACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1293
 QY 842 AGCACTGCTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 901
 DB 1294 AATTCATGAGAGCATGATGATGATGATGATGATGATGATGATGATGATGAT 1353
 QY 902 GATTTCTTATTTGTCAGCATATGATGATGATGATGATGATGATGATGATGAT 955
 DB 1354 CGGGATTTTGTGTTTATATTAATAAATGATGATGATGATGATGATGATGATGAT 1407

RESULT 15

AAH66357
ID AAH66357 standard; DNA; 1005 BP.

XX AAH66357;

XX 26-SEP-2001 (first entry)

XX C glutamicum coding sequence fragment SEQ ID NO: 1392.

XX Coryneform bacterium; amino acid synthesis; vitamin; saccharide;

XX organic acid synthesis; ds.

XX Corynebacterium glutamicum.

XX EP1108790-A2.

XX 20-JUN-2001.

XX 18-DEC-2000; 2000EP-0127688.

XX 16-DEC-1999; 99JP-0377484.

XX 07-APR-2000; 2000JP-0159162.

XX 03-AUG-2000; 2000JP-0280988.

XX (KYOWA) KYOWA HAKKO KOGYO KK.

XX Nakagawa S, Mizoguchi H, Ando S, Hayaashi M, Ochiai K, Yokoi H;

XX Tateishi N, Senoh A, Ikeda M, Ozaki A;

XX WPI; 2001-376931/40.

XX P-PSDB; AAC91138.

XX Claim 8: SEQ ID NO: 1392; 246bp + Sequence Listing; English.

CC The present invention provides a number of nucleotide and protein
 CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of coryneform bacterium, measuring expression amount and
 CC analysing the expression profile or expression pattern of a gene derived
 CC from Coryneform bacterium, and identifying a homologue of a gene derived
 CC from coryneform bacterium. Coryneform bacteria are useful for producing
 CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a nucleic acid described
 CC in the exemplification of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC European Patent Office.

XX Sequence 1005 BP; 179 A; 284 C; 261 G; 281 T; 0 other;

XX Query Match 4.7%; Score 53.6; DB 22; Length 1005;

XX Best Local Similarity 47.4%; Pred. No. 5.3e-06;

XX Matches 161; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

QY 89 TGGAGCTCGTTTTCACAGTGTGTCACATGTGATGATGGGGCTGCTGATGTTCTTTGG 148

DB 122 TTGTGTCATATTTCTTGTGGTCAATCCTTGTGGGCAATCATGATGTTCTTCATGG 181

QY 149 GATGTTCCGTGAGATCCGAGACTGTGTGCACATCAGAGACCTGGGGCATTCGTCG 208

DB 182 GCTGACCTTGAAGCCAGTGAATGACCTTGTGCTAAAGCCACATCCAGTTCTTA 241

QY 209 TGGAGCTGCTGCTGCGAGTTTGGGCTCATGCTTTTACAGTTATCTCGGCCATTAGCT 268

DB 242 TCGGCGTGAATCGCCAGTTTGTGATCATGATCCCTGATGCAATGCTGTGAGTTT 301

QY 269 TTTCTGAGCCAGTCCAGCTATTTGCTGTTCTTCATCATGAGGCTGTGCCCGGGGCA 328
 DB 302 TGCAGCTGCTGCGGAAATTTGCGGCGGTGTGATCTTGTGTGTCACCTGGCGGAA 361
 QY 329 CCATCTTAACATTTTCACTTTGAGTTGATGAGATATGATCTCAGCATCATGA 388
 DB 362 CTTCCTCAACGTGTGTTTAACTGTCCGCTGATGATGTCGCTGTGTCACCATGA 421
 QY 389 CAACCTGTTCACCGTGGCGCCCTTGGGATGATGCACT 428
 DB 422 CTTCATCTCAGCTGCTGTGCTCAATTTTCACTCACT 461

Search completed: June 9, 2003, 05:35:48
 Job time : 305 secs